



## eTBLAST: a text-similarity based search engine

[Home](#)[ARCH](#)[Deja Vu](#)[Pair  
Comparison](#)[For clients](#)[My eTBLAST](#)[APIs](#)[Quick Guide](#)[View query](#) [Query log records](#)

## Analyze the results with a post-processor:

[Quick Guide  
Support of eTBLAST](#)[Find Expert](#)[Find Journal](#)[Publication History](#)[Implicit Keywords](#)[Similarity Matrix of Top Hits](#)

## Most Similar Matches in MEDLINE:

Score of self comparison: 103.997

- |    |  |                             |
|----|--|-----------------------------|
| 1  | <a href="#">DNA amplification method tolerant to sample degradation.</a>   | Score: 94.2<br>Ratio: 0.91  |
|    | G Wang, E Maher, C Brennan, L Chin, C Leo, M Kaur, P Zhu, M Rook, JL Wolfe, GM Makrigiorgos. Genome research, 2004, Nov., 14(11): 2357-66. PMID: 15520297  |                             |
| 2  | <a href="#">Evaluation of affinity-based genome-wide DNA methylation data: Effects of CpG density, amplification bias, and copy number variation.</a>  | Score: 92.15<br>Ratio: 0.89 |
|    | MD Robinson, C Strzaker, AL Statham, MW Coolen, JZ Song, SS Nair, D Stibenac, TP Speed, SJ Clark. Genome research, 2010, Dec., 20(12): 1719-29. PMID: 21045081   |                             |
| 3  | <a href="#">Critical regions identify genome-wide DNA methylation profiles.</a>  | Score: 78.55<br>Ratio: 0.76 |
|    | GE Ananiev, S Goldstein, R Runnheim, DK Forrest, S Zhou, K Potamocous, CP Churns, V Bergendahl, JA Thomson, DC Schwartz. BMC molecular biology, 2008., 9(): 68. PMID: 18667073   |                             |
| 4  | <a href="#">Isolation of whole genome amplification from single and small numbers of cells: a new era for preimplantation genetic diagnosis of inherited disease.</a>  | Score: 73.55<br>Ratio: 0.71 |
|    | AH Handyside, MD Robinson, RJ Simpson, MB Omar, MA Shaw, JG Grudzinskas, A Rutherford. Molecular human reproduction, 2004, Oct., 10(10): 767-72. PMID: 15322224  |                             |
| 5  | <a href="#">Whole genome amplification: applications and advances.</a>   | Score: 71.96<br>Ratio: 0.69 |
|    | TL Hawkins, JC Detter, PM Richardson. Current opinion in biotechnology, 2002, Feb., 13(1): 65-7. PMID: 11849960  |                             |
| 6  | <a href="#">Specific and complete human genome amplification with improved solid supports by phi29 DNA polymerase and a novel primer at degraded microarrays.</a>  | Score: 68.26<br>Ratio: 0.66 |
|    | O Aismadi, F Alkayal, D Monies, BF Meyer. BMC research notes, 2009., 2(): 48. PMID: 19309528   |                             |
| 7  | <a href="#">HLA class II typing of whole genome amplified menarcheal DNA.</a>  | Score: 64.94<br>Ratio: 0.62 |
|    | KM Gillespie, SJ Valovin, JA Saubly, KM Hunter, DA Savage, D Middleton, JA Todd, PJ Bingley, EA Gale. Tissue antigens, 2000, Dec., 56(6): 530-8. PMID: 11169243  |                             |
| 8  | <a href="#">Quantitative analysis of DNA methylation after whole blood fractionation and amplification of a minute amount of DNA from body fluids.</a>   | Score: 60.62<br>Ratio: 0.58 |
|    | T Valastro, C Cunin, A Palival, P Vincis, G Hook, M Krzyzanowski, L Airola, A Dunning, S Garte, P Hainaut, C Malaveille, K Overvad, F Clavel-Chapelon, J Lissenes, H Boeing, A Trichopoulos, D Trichopoulos, A Kalladidi, D Palli, V Krogh, R Tumino, S Panico, HB Bueno-De-Mesquita, PH Peeters, M Kumle, CA Gonzalez, C Martinez, M Dorronsoro, A Barriacane, C Navarro, JR Quirós, G Berglund, I Janson, B Jarvholm, NE Day, TJ Key, R Saracci, R Kaaks, E Riboli, P Hainaut, Z Herceg. Epigenetics : official journal of the DNA Methylation Society, 2009, May., 4(4): 221-30. PMID: 19458486 |                             |
| 9  | <a href="#">Assessment of whole genome amplification obtained by bisulfite high throughput massively parallel whole genome sequencing.</a>   | Score: 60.58<br>Ratio: 0.58 |
|    | R Pinard, A de Winter, GJ Sarkis, MB Gerstein, KR Turtaro, RN Plant, M Egholm, JM Rothberg, JH Leamon. BMC genomics, 2006., 7(): 216. PMID: 16928277   |                             |
| 10 | <a href="#">A whole-genome amplification protocol for a wide variety of DNAs, including those from formalin-fixed and paraffin-embedded tissue.</a>  | Score: 59.86<br>Ratio: 0.58 |
|    | PL Paris. Methods in molecular biology (Clifton, N.J.), 2009., 556(): 89-98. PMID: 19488873  |                             |
| 11 | <a href="#">Perspective of DNA methylation in forensic genetics and new promises of its detection methods.</a>   | Score: 58.86<br>Ratio: 0.57 |
|    | SM Zhao, CT Li. Fa yi xue za zhi, 2009, Aug., 25(4): 290-5. PMID: 19788082   |                             |

Relevancy Threshold (Similarity ratio = 0.50). Entries above here have an unusual level of similarity

12	<a href="#">Methylation perturbations in neurodegeneration within the genome of a <i>Mus musculus</i> hybrid correlate with de novo minute chromosome formation</a> JD Brown, D Golden, RJ O'Neill. Genomics, 2008, Mar., 91(3): 267-73. PMID: 18226492	Score: 58.31 Ratio:0.56
13	<a href="#">Evaluation of whole-genome amplification using multiple displacement amplification of a limited number of cells.</a> S Bushardes, N Salame, PC Patsalis. Clinical chemistry and laboratory medicine : CCLM / FESCC, 2006, , 44(9): 1158-60. PMID: 16958614	Score: 57.84 Ratio:0.56
14	<a href="#">Evaluation of whole genome amplification methods for array and oligonucleotide CVD.</a> A Hittelman, S Sridharan, R Roy, J Fridlyand, M Loda, C Collins, PL Paris. Diagnostic molecular pathology : the American journal of surgic, 2007, Dec., 16(4): 196-206. PMID: 18043282	Score: 57.27 Ratio:0.55
15	<a href="#">Whole genome amplification of the rat <i>Escherichia coli</i> L. on. viridis from single cells.</a> Y Wang, M Zhu, R Zhang, H Yang, Y Wang, G Sun, S Jin, T Hsiang. Journal of microbiological methods, 2009, May., 77(2): 229-34. PMID: 19235233	Score: 56.54 Ratio:0.54
16	<a href="#">A whole genome amplification method to generate long fragments from low quantities of genomic DNA.</a> R Kitter, M Stoneking, M Kayser. Analytical biochemistry, 2002, Jan., 300(2): 237-44. PMID: 11779116	Score: 56.34 Ratio:0.54
17	<a href="#">Whole genome amplification of eukaryotic whole-genome DNA allows for accurate estimates of methylated cytosine density in targeted DNA sequences.</a> J Mill, S Yazdani, E Gückel, S Ziegler, Z Kaminsky, A Petronis. BioTechniques, 2006, Nov., 41(5): 603-7. PMID: 17140118	Score: 55.81 Ratio:0.54
18	<a href="#">Determination of the global DNA methylation status of rat according to the identifier repetitive elements.</a> HH Kim, JH Park, KS Jeong, S Lee. Electrophoresis, 2007, Nov., 28(21): 3854-61. PMID: 17960839	Score: 55.81 Ratio:0.54
19	<a href="#">Profiling DNA methylation from small amounts of genomic DNA using a microfluidic sodium bisulfite conversion and subsequent whole genome amplification.</a> J Mill, A Petronis. Methods in molecular biology (Clifton, N.J.), 2009, , 507(3): 371-81. PMID: 18987828	Score: 55.61 Ratio:0.53
20	<a href="#">Analysis of DNA methylation by amplification of unmethylated sites (AIMS).</a> M Jordá, J Rodríguez, J Frigola, MA Peinado. Methods in molecular biology (Clifton, N.J.), 2009, , 507(3): 107-16. PMID: 18987810	Score: 54.05 Ratio:0.52
21	<a href="#">Genome-wide divergence of DNA methylation marks in conserved and nonconserved contexts.</a> Y Xin, B Chanion, MM Liu, H Gafalvy, R Costa, B Ilievski, G Rosoklija, V Arango, AJ Dwork, J Mann, B Tycko, F Haghighi. PloS one, 2010, , 5(6): e11357. PMID: 20596539	Score: 53.68 Ratio:0.52
22	<a href="#">SNP-based chromosome copy number determination following multiple displacement whole-genome amplification.</a> JJ Comeveaux, MC Krue, D Hu-Lince, KE Ramsey, VI Zismann, DA Stephan, DW Craig, MJ Hueltner. BioTechniques, 2007, Jan., 42(1): 77-83. PMID: 17269488	Score: 53.67 Ratio:0.52
23	<a href="#">A genome-wide survey of brain DNA methylation identifies new candidate genes for sporadic amyotrophic lateral sclerosis.</a> JM Morahan, B Yu, RJ Trent, R Pamphlett. Amyotrophic lateral sclerosis : official publication of the Wor., , 10(5-6): 418-29. PMID: 19922134	Score: 53.39 Ratio:0.51
24	<a href="#">High-throughput profiling of the H19 differentially methylated region and comprehensive whole genome array-based analysis in Silico-chuvali syndrome.</a> SY Lin, CN Lee, CC Hung, WY Tsai, SP Lin, NC Li, WS Hsieh, YC Tung, DM Niu, WM Hsu, LY Chen, MY Yang, MP Tu, PW Kuo, CY Lin, YN Su, HN Ho. American journal of medical genetics. Part A, 2010, Oct., 152A(10): 2521-8. PMID: 20830799	Score: 53.36 Ratio:0.51
25	<a href="#">The use of multiple displacement amplified DNA as a control for methylation specific PCR, pyrosequencing, bisulfite sequencing and methylation sensitive restriction enzyme PCR.</a> S Hughes, JL Jones. BMC molecular biology, 2007, , 8(1): 91. PMID: 17959862	Score: 52.66 Ratio:0.51
26	<a href="#">Minimizing the genome size using whole genome amplification.</a> J Yazaki, BD Gregory, JR Ecker. Current opinion in plant biology, 2007, Oct., 10(5): 534-42. PMID: 17703988	Score: 51.34 Ratio:0.49
27	<a href="#">Synthesis of universal unamplified genomic DNA by nested whole genome amplification using phi29 DNA polymerase.</a> N Umetsu, M de Maat, T Mori, H Takeuchi, DS Hoon. Biochemical and biophysical research communications, 2005, Apr., 329(1): 219-23. PMID: 15721296	Score: 51.27 Ratio:0.49
28	<a href="#">Genetic software to design primers optimized for whole genome scanning by long-range PCR amplification.</a> N Ben Zakour, M Gaudier, R Andonov, D Lavenier, MF Cochet, P Veber, A Sorokin, Y Le Loir. Nucleic acids research, 2004, , 32(1): 17-24. PMID: 14704339	Score: 49.63 Ratio:0.48
29	<a href="#">Mutations of TR-53 reduce loss of DNA methylation and specification of the TROP1 gene.</a> AF Nasr, M Nutini, B Palombo, E Guerra, S Alberici. Oncogene, 2003, Mar., 22(11): 1668-77. PMID: 12642870	Score: 49.41 Ratio:0.48

30	<a href="#">The separation, lysis, and DNA methylation</a> J Geisel, H Schorr, M Bodis, S Isler, U Hubner, JP Knapp, R Obcid, W Herrmann. Clinical chemistry and laboratory medicine : CCLM / FESCC, 2005, , 43(10): 1164-9. PMID: 16197315	Score: 49.1 Ratio:0.47
31	<a href="#">Two new methods of whole-genome amplification enable accurate genotyping across a 1.22-Mb SNP linkage panel</a> DL Barker, MS Hansen, AF Faruqi, D Giannola, OR Insula, RS Lasken, M Lattierich, V Makarov, A Oliphant, JH Pinter, R Shen, I Steptsova, W Ziehl, E Lai. Genome research, 2004, May, , 14(5): 901-7. PMID: 15123587	Score: 48.47 Ratio:0.47
32	<a href="#">Sequencing of the large ddDNA genome of <i>Oryctolagus cuniculus</i> using multiple displacement amplification of nonrandom regions of viral DNA</a> Y Wang, RG Kleespies, MB Ramle, JA Jehle. Journal of virological methods, 2008, Sep, , 152(1-2): 106-8. PMID: 18598718	Score: 47.45 Ratio:0.46
33	<a href="#">Whole genome amplification with Pfu220 DNA polymerase to enable genetic or genomic analysis of samples of low DNA yield</a> K Silander, J Saarela. Methods in molecular biology (Clifton, N.J.), 2008, , 439(): 1-18. PMID: 18370092	Score: 46.96 Ratio:0.45
34	<a href="#">Whole genome amplification on poly(dimethylsiloxane) microchip arrays</a> L Chen, A Manz, PJ Day. Analytical biochemistry, 2008, Jan, , 372(1): 128-30. PMID: 17949674	Score: 45.11 Ratio:0.43
35	<a href="#">Applications of DNA array arrays for whole genome analysis</a> TC Mockler, S Chan, A Sundaresan, H Chen, SE Jacobsen, JR Ecker. Genomics, 2005, Jan, , 85(1): 1-15. PMID: 15607417	Score: 44.51 Ratio:0.43
36	<a href="#">Whole genome multiple displacement amplification from single cells</a> C Spits, C Le Cañgnet, M De Rycke, L Van Haute, A Van Steirteghem, I Liebaers, K Sermon. Nature protocols, 2006, , 1(4): 1965-70. PMID: 17487184	Score: 44.09 Ratio:0.42
37	<a href="#">Restriction landmark genome scanning</a> JF Costello, DJ Smiraglia, C Plass. Methods (San Diego, Calif.), 2002, Jun, , 27(2): 144-9. PMID: 12095273	Score: 43.53 Ratio:0.42
38	<a href="#">From molecular detection for the prevention of tumor and degenerative diseases: epigenetic DNA methylation</a> G De Palma, P Mozzoni. Giornale italiano di medicina del lavoro ed ergonomia, , 31(1): 51-3. PMID: 19558040	Score: 42.47 Ratio:0.41
39	<a href="#">Genome-wide association of histone H3 by <i>in situ</i> non-methylation with C-H3 DNA methylation in <i>Arabidopsis thaliana</i></a> YV Bernatavichute, X Zhang, S Cokus, M Pellegrini, SE Jacobsen. PloS one, 2008, , 3(9): e3156. PMID: 18776934	Score: 42.36 Ratio:0.41
40	<a href="#">Whole genome amplification and de novo assembly of single bacterial cells</a> S Rodrigue, RR Malmstrom, AM Berlin, BW Birren, MR Henn, SW Chisholm. PloS one, 2009, , 4(9): e6864. PMID: 19724646	Score: 41.22 Ratio:0.4
41	<a href="#">Highly efficient PCR assay to discriminate stable DNA methylation status using whole genome amplification</a> Y Yamada, T Ito. BMC research notes, 2011, , 4(): 179. PMID: 21663670	Score: 41.18 Ratio:0.4
42	<a href="#">Evaluation of 2 methods of whole genome amplification for subsequent microarray comparative genomic hybridization</a> G Ng, I Roberts, N Coleman. Diagnostic molecular pathology : the American journal of surg, 2005, Dec, , 14(4): 203-12. PMID: 16319690	Score: 41.17 Ratio:0.4
43	<a href="#">Detection and analysis of mitochondrial DNA deletions by whole genome PCR</a> CH Tengan, CT Moraes. Biochemical and molecular medicine, 1996, Jun, , 58(1): 130-4. PMID: 8809354	Score: 39.35 Ratio:0.38
44	<a href="#">Massive DNA sequencing strategies and genome assemblies</a> RJ Okagaki, RL Phillips. Genome biology, 2004, , 5(5): 223. PMID: 15128439	Score: 39.2 Ratio:0.38
45	<a href="#">Stable <i>in vivo</i> specific CpG methylation of DNA in <i>Caenorhabditis elegans</i></a> TL Azhikina, ED Sverdlov. Biochemistry. Biokhimiya, 2005, May, , 70(5): 596-603. PMID: 15948713	Score: 39.1 Ratio:0.38
46	<a href="#">Whole genome amplification from a single cell: applications for research and analysis</a> L Zhang, X Cui, K Schmitt, R Hubert, W Navid, N Arnheim. Proceedings of the National Academy of Sciences of the United S, 1992, Jul, , 89(13): 5847-51. PMID: 1631067	Score: 39 Ratio:0.37
47	<a href="#">Whole genome amplification: abundant varieties of DNA from precious samples or clinical specimens</a> RS Lasken, M Egholm. Trends in biotechnology, 2003, Dec, , 21(12): 531-5. PMID: 14624861	Score: 37.59 Ratio:0.36
48	<a href="#">Fidelity of whole genome amplification of blood spot DNA on HPA typing and SNP analysis</a> KK Singh, SA Spector. Clinical genetics, 2007, Aug, , 72(2): 156-9. PMID: 17661821	Score: 37.59 Ratio:0.36
49	<a href="#">Whole genome amplification of DNA from residual cells left by accidental contact</a>	Score: 37.59 Ratio:0.36

	KJ Sorensen, K Turteltaub, G Vrankovich, J Williams, AT Christian. Analytical biochemistry, 2004, Jan., 324(2): 312-4. PMID: 14690700	
50	<a href="#">Improved efficiency of whole genome amplification from bacterial cells.</a> YM Kwon, MM Cox. BioTechniques, 2004, Jul., 37(1): 40, 42, 44. PMID: 15283198	Score: 37.59 Ratio:0.36
51	<a href="#">Genome-wide, high-resolution DNA methylation profiling using bisulfite-mediated cytosine conversion.</a> J Reinders, C Delucinge Vivier, G Theiler, D Chollet, P Descombes, J Paszkowski. Genome research, 2008, Mar., 18(3): 469-76. PMID: 18218979	Score: 37.38 Ratio:0.36
52	<a href="#">Whole genome amplification of plasma-circulating DNA enables expanded screening for genetic biomarkers in plasma.</a> J Li, L Harris, H Mamon, MH Kulke, WH Liu, P Zhu, G Mike Makrigiorgos. The Journal of molecular diagnostics : JMD, 2006, Feb., 8(1): 22-30. PMID: 16436631	Score: 37.18 Ratio:0.36
53	<a href="#">Amplification of bisulfite-converted DNA for genome-wide DNA methylation profiling.</a> J Reinders. Cold Spring Harbor protocols, 2009, Dec., 2009(12): pdb.prot5342. PMID: 20150089	Score: 36.93 Ratio:0.36
54	<a href="#">Genome-wide assays using amplified material from blood spot samples.</a> MV Hollegaard, J Graubolm, A Berghum, M Nyegaard, B Nørgaard-Pedersen, T Ørntoft, PB Mortensen, C Wiuf, O Mors, M Didriksen, P Thomsen, DM Hougaard. BMC genomics, 2009, , 10( ): 297. PMID: 19575812	Score: 36.46 Ratio:0.35
55	<a href="#">Whole-genome amplification of oral tissue cell-collected DNA in a population-based case-control study of breast cancer.</a> X Liang, A Trentham-Dietz, L Tius-Ernstoft, PA Newcomb, RA Welch, AA Hutchinson, JM Hampton, CB Sutcliffe, JL Haines, KM Egan. Cancer epidemiology, biomarkers prevention : a publication of the American Association for Cancer Research, 2007, Aug., 16(8): 1610-4. PMID: 17684135	Score: 36.46 Ratio:0.35
56	<a href="#">Visual genome scan: a tool for consistent landmark-based analysis of the human genome.</a> JM Rouillard, AE Erson, R Kuick, J Asakawa, K Wimmer, M Muleris, EM Petty, S Hanash. Genome research, 2001, Aug., 11(8): 1453-9. PMID: 11483587	Score: 36.39 Ratio:0.35
57	<a href="#">Multitube primed rolling-circle amplification method for the amplification of circular DNA viruses.</a> H Stevens, A Rector, M Van Ranst. Cold Spring Harbor protocols, 2010, Apr., 2010(4): pdb.prot5415. PMID: 20360369	Score: 36.06 Ratio:0.35
58	<a href="#">Study on application of the whole genome amplification in LCN.</a> HG Zhou, C Zhang. Fa yi xue za zhi, 2006, Feb., 22(1): 43-4, 47. PMID: 16524185	Score: 35.74 Ratio:0.34
59	<a href="#">Bovine microsatellite genome amplification for genomic characterization of filarial parasites.</a> SN McNulty, GJ Weil, M Heinz, SD Crosby, PU Fischer. Experimental parasitology, 2008, Jun., 119(2): 256-63. PMID: 18359019	Score: 35.63 Ratio:0.34
60	<a href="#">Detection of cytosine methylation and mapping of a gene influencing cytosine methylation in the genome of China.</a> Q Cai, CL Guy, GA Moore. Genome / National Research Council Canada = Genome / Conseil na, 1996, Apr., 39(2): 235-42. PMID: 8984000	Score: 34.38 Ratio:0.33
61	<a href="#">Singleton birth after retransplantation genetic diagnosis for thymosin disease using whole genome amplifications.</a> JF Chow, WS Young, EY Lau, ST Lam, T Tong, EH Ng, PC Ho. Fertility and sterility, 2009, Aug., 92(2): 828.e7-10. PMID: 19515365	Score: 34.34 Ratio:0.33
62	<a href="#">Rolling-circle amplification of viral DNA genomes using phi29 polymerase.</a> R Johe, H Müller, A Rector, M van Ranst, H Stevens. Trends in microbiology, 2009, May., 17(5): 205-11. PMID: 19375325	Score: 34.04 Ratio:0.33
63	<a href="#">Primer design for whole genome amplification using genetic algorithms.</a> AE Ping, KW Choo, CI Lee, SH Leong, OL Kon. In silico biology, 2006, , 6(6): 505-14. PMID: 17518761	Score: 33.69 Ratio:0.32
64	<a href="#">Application of whole genome amplification and quantitative PCR for detection and quantification of spore-forming bacteria in ground beef.</a> A Renard, P Gómez de Marco, M Egea-Cortines, J Weiss. International journal of food microbiology, 2008, Aug., 126(1-2): 195-201. PMID: 18597878	Score: 33.14 Ratio:0.32
65	<a href="#">DNA methylation and the functional organization of the nuclear compartment.</a> J Espada, M Esteller. Seminars in cell developmental biology, 2010, Apr., 21(2): 238-46. PMID: 19892028	Score: 31.57 Ratio:0.3
66	<a href="#">Whole genome amplification and genetic analysis after extraction of nucleic acids from dried blood spots.</a> MV Hollegaard, KM Sorensen, HK Petersen, MB Armadotir, B Nørgaard-Pedersen, P Thomsen, DM Hougaard. Clinical chemistry, 2007, Jun., 53(6): 1161-2. PMID: 17517589	Score: 30.07 Ratio:0.29
67	<a href="#">Self-priming primer to modified random octanucleotide facilitates the quality control of whole genome amplification.</a> I Brukner, B Paquin, M Belouchi, D Labuda, M Kraljicovic. Analytical biochemistry, 2005, Apr., 339(2): 345-7. PMID: 15797576	Score: 30.07 Ratio:0.29
68	<a href="#">Comparing whole-genome amplification methods and studies of biological samples for single-nucleotide polymorphism genotyping.</a>	Score: 30.07 Ratio:0.29

	JW Park, TH Beatty, P Boyce, AF Scott, I McIntosh. <i>Clinical chemistry</i> , 2005, Aug., 51(8): 1520-3. PMID: 16040848	
69	<a href="#">[16] <i>In situ ethylation of phorbate for ex vivo DNA methylation level of genes in the nucleus latus</i></a>	Score: 29.85 Ratio:0.29
	SD Wu, J Zhu, YS Li, LQ Gan, XG Yuan, MD Xu, GH Wei. <i>Zhonghua nan ke xue = National journal of andrology</i> , 2009, Oct., 15(10): 876-81. PMID: 20112733	
70	<a href="#">[17] <i>Comprehensive human genome amplification using multiple displacement amplification</i></a>	Score: 29.65 Ratio:0.29
	FB Dean, S Hosono, I Fang, X Wu, AF Faruqi, P Bray-Ward, Z Sun, Q Zeng, Y Du, J Du, M Driscoll, W Song, SF Kingsmore, M Egholm, RS Lasken. <i>Proceedings of the National Academy of Sciences of the United S</i> , 2002, Apr., 99(8): 5261-6. PMID: 11959976	
71	<a href="#">[18] <i>Variable patterns of total DNA and dDNA methylation in animals</i></a>	Score: 28.4 Ratio:0.27
	AP Bird, MH Taggart. <i>Nucleic acids research</i> , 1980, Apr., 8(7): 1485-97. PMID: 6253937	
72	<a href="#">[19] <i>Enriched isothermal amplification of the entire genome from single cells</i></a>	Score: 27.8 Ratio:0.27
	KV Schowater, J Fredrickson, AR Thornhill. <i>Methods in molecular medicine</i> , 2007, , 132(): 87-99. PMID: 17876078	
73	<a href="#">[20] <i>Whole genome amplification of single cells: mathematical analysis on FSP and tagged PCR</i></a>	Score: 27.19 Ratio:0.26
	F Sun, N Arheim, MS Waterman. <i>Nucleic acids research</i> , 1995, Aug., 23(15): 3034-40. PMID: 7659528	
74	<a href="#">[21] <i>Twofold the number of the genome of single cells: further characterization of the multiple displacement amplification</i></a>	Score: 25.8 Ratio:0.25
	S Panelli, G Dumiani, L Espen, G Micheli, V Sgarbetta. <i>Gene</i> , 2006, May., 372(): 1-7. PMID: 16564650	
75	<a href="#">[22] <i>A whole-genome mass BAC microarray with 1-Mb resolution for analysis of DNA copy number changes by array comparative genomic hybridization</i></a>	Score: 25.05 Ratio:0.24
	YJ Chung, J Jonkers, H Kitson, H Fiegler, S Humphray, C Scott, S Hunt, Y Yu, I Nishijima, A Velds, H Holstege, N Carter, A Bradley. <i>Genome research</i> , 2004, Jan., 14(1): 188-96. PMID: 14707179	
76	<a href="#">[23] <i>Whole-genome microarray using laser microdissection device</i></a>	Score: 24.65 Ratio:0.24
	CM Felmette, SC Mok. <i>Methods in molecular biology</i> (Clifton, N.J.), 2005, , 293(): 69-77. PMID: 16028411	
77	<a href="#">[24] <i>BSMAF: whole genome bacterial sequence mapping program</i></a>	Score: 23.99 Ratio:0.23
	Y Xi, W Li. <i>BMC bioinformatics</i> , 2009, , 10(): 232. PMID: 19635165	
78	<a href="#">[25] <i>The amplification and high efficient cloning of the whole genome sequence of hepatitis B virus</i></a>	Score: 23.48 Ratio:0.23
	BY Xu, YM Wang, L Lang, YP Huang. <i>Zhonghua gan zang bing za zhi = Zhonghua ganzhangbing zazhi = Ch</i> , 2005, Sep., 13(9): 704-6. PMID: 16174469	
79	<a href="#">[26] <i>Preparation of genome-wide DNA fragment libraries using bisulfite in polyacrylamide gel electrophoresis gels with formaldehyde denaturation and quality control for massively parallel sequencing by oligonucleotide ligation and detection</i></a>	Score: 23.22 Ratio:0.22
	SS Ranade, CB Chung, G Zou, VL Boyd. <i>Analytical biochemistry</i> , 2009, Jul., 390(2): 126-35. PMID: 19379703	
80	<a href="#">[27] <i>Analysis and accurate quantification of CpG methylation by MALDI mass spectrometry</i></a>	Score: 21.96 Ratio:0.21
	J Tost, P Schatz, M Schuster, K Berlin, IG Gut. <i>Nucleic acids research</i> , 2003, May., 31(9): e50. PMID: 12711695	
81	<a href="#">[28] <i>Preimplantation genetic diagnosis of Marfan syndrome using multiple displacement amplification</i></a>	Score: 21.62 Ratio:0.21
	B Liedó, J Ten, FM Galán, R Bernabeu. <i>Fertility and sterility</i> , 2006, Oct., 86(4): 949-55. PMID: 17027361	
82	<a href="#">[29] <i>Evaluation of whole genome amplification methods using pseudogenes from samples</i></a>	Score: 21.57 Ratio:0.21
	K Iwamoto, J Ueda, Y Nakano, M Bando, W Ukai, E Hashimoto, T Saito, T Kato. <i>Journal of neuroscience methods</i> , 2007, Sep., 165(1): 104-10. PMID: 17604841	
83	<a href="#">[30] <i>Non-saturating and Non-specific microarrays to detect copy number and methylation changes in whole genomes</i></a>	Score: 21.46 Ratio:0.21
	J Li, A Protopopov, F Wang, V Senchenko, V Peshkov, O Vorontsova, L Peterenko, V Zharovskaya, O Muravenko, E Braga, I Kisselev, MI Lerman, V Kasubha, G Klein, I Ernberg, G Wahlestedt, ER Zharovskiy. <i>Proceedings of the National Academy of Sciences of the United S</i> , 2002, Aug., 99(16): 10724-9. PMID: 12149436	
84	<a href="#">[31] <i>Genetic identity of clones and methods to explore DNA</i></a>	Score: 20.68 Ratio:0.2
	B de Montier, I Boulanger, S Taurin, JP Renard, A Eggen. <i>Cloning and stem cells</i> , 2004, , 6(2): 133-9. PMID: 15268787	
85	<a href="#">[32] <i>Genome de novo and DNA methylation in Neurospora</i></a>	Score: 20.62 Ratio:0.2
	EU Selker. <i>Cold Spring Harbor symposia on quantitative biology</i> , 2004, , 69(): 119-24. PMID: 16117640	
86	<a href="#">[33] <i>Whole methylation analysis by ultra-deep sequencing using next-generation sequencing</i></a>	Score: 20.57 Ratio:0.2
	CA Bormann Chung, VL Boyd, KJ McKernan, Y Fu, C Monighetti, HE Peckham, M Barker. <i>PLoS one</i> , 2010, , 5(2): e9320. PMID: 20179767	
87	<a href="#">[34] <i>Amplifying whole genomes with multiple displacement amplification</i></a>	Score: 19.93 Ratio:0.19

	N Gorrochategui-Escalante, WC Black. Insect molecular biology, 2003, Apr., 12(2): 195-200. PMID: 12653941	
88	<a href="#">Amplification of fungal genomes using multiple displacement amplification.</a>	Score: 19.69 Ratio:0.19
	SI Foster, BJ Monahan. Methods in molecular biology (Clifton, N.J.), 2010, , 638(0): 175-85. PMID: 20238269	
89	<a href="#">Nanopore cytosine extension assay: a highly sensitive method to evaluate CpG island methylation in the whole genome.</a>	Score: 19.48 Ratio:0.19
	H Fujiwara, M Ito. Analytical biochemistry, 2002, Aug., 307(2): 386-9. PMID: 12202260	
90	<a href="#">Complete mitochondrial genome amplification.</a>	Score: 18.58 Ratio:0.18
	S Cheng, R Higuchi, M Sioneking. Nature genetics, 1994, Jul., 7(3): 350-1. PMID: 7920652	
91	<a href="#">Methylation profiling of cancer cells by amplification of 5methylcytosine (5mC).</a>	Score: 18.53 Ratio:0.18
	J Frigola, M Ribas, RA Risques, MA Peinado. Nucleic acids research, 2002, Apr., 30(7): e28. PMID: 11917034	
92	<a href="#">Implementation of genome amplification technology for 18S rRNA detection.</a>	Score: 16.26 Ratio:0.16
	R Eglin. Transfusion medicine (Oxford, England), 2002, Aug., 12(4): 265-73. PMID: 12220256	
93	<a href="#">Amplification of Ato family in forensic DNA analysis.</a>	Score: 15.51 Ratio:0.15
	GS Zhao, L Chang, YN Mo. Fa yi xue za zhi, 2010, Feb., 26(1): 47-50. PMID: 20232745	
94	<a href="#">Whole-genome deconvolution.</a>	Score: 14.85 Ratio:0.14
	P Green. Proceedings of the National Academy of Sciences of the United S, 2002, Apr., 99(7): 4143-4. PMID: 11904394	
95	<a href="#">Assessing a whole-genome shotgun.</a>	Score: 14.85 Ratio:0.14
	P Green. Genome research, 1997, May., 7(5): 410-7. PMID: 9149937	
96	<a href="#">A whole genome shotgun in the ESTM project.</a>	Score: 14.85 Ratio:0.14
	M Itaya, K Tsuge, M Koizumi, K Fujita. Tanpakushitsu kakusan koso. Protein, nucleic acid, enzyme, 2006, Jan., 51(1): 61-7. PMID: 16416884	
97	<a href="#">Whole rDNA genome typing.</a>	Score: 14.85 Ratio:0.14
	U Römeling, D Grothues, B Tümmler. Antibiotics and chemotherapy, 1991, , 44(0): 1-7. PMID: 1801627	
98	<a href="#">Methicillin-resistant, modeling a mosaicable genome.</a>	Score: 10.12 Ratio:0.1
	JM Ordway, T Curran. Cell growth differentiation : the molecular biology journal o, 2002, Apr., 13(4): 149-62. PMID: 11971815	
99	<a href="#">Phi29-based amplification of small genomes.</a>	Score: 8.73 Ratio:0.08
	I Brukner, D Labuda, M Kraljovic. Analytical biochemistry, 2006, Jul., 354(1): 154-6. PMID: 16701073	
100	<a href="#">Gene amplification: an example of genome rearrangement.</a>	Score: 8.73 Ratio:0.08
	C Delidakis, C Swimmer, FC Kafatos. Current opinion in cell biology, 1989, Jan., 1(3): 488-96. PMID: 2697268	

## Your query:

(

[Query keywords](#)

## Statistics Summary:

# total number of words in submitted query:5  
# total number of keywords in submitted query:5  
# query start at:2011-12-18 22:21:35  
# computation time:2 seconds  
# total number of matched documents:100  
# total number of documents in MEDLINE:19667033

About eTBLAST: [Help](#) | [Disclaimer](#) | [Contact](#) | Copyright © 2001 - 2011